

DT05 Rec'd PCT/PTO 18 FEB 2005

SEQUENCE LISTING

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 Schopfer, Christel R

<120> Process for preparing ketocarotenoids in genetically modified organisms

<130> 13173-00006-US

<150> PCT/EP2003/009106
 <151> 2003-08-18

<150> DE 102 38 980.2
 <151> 2002-08-20

<150> DE 102 38 978.0
 <151> 2002-08-20

<150> DE 102 38 979.9
 <151> 2002-08-20

<150> DE 102 53 112.9
 <151> 2002-11-13

<150> DE 102 58 971.2
 <151> 2002-12-16

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<170> PatentIn version 3.3

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Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn	
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ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa	336
Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys	
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115 120 125	
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195 200 205	
ggg tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt	672
Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe	
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Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His	
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50 55 60

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
65 70 75 80

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
100 105 110

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
115 120 125

Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
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165 170 175

Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
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Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
195 200 205

Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

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 Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
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 Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
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tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa 192
 Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60

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 Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
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 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95

cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag 336
 Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110

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Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe			
130	135	140	
atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta			480
Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu			
145	150	155	160
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc			528
Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile			
165	170	175	
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ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat			624
Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr			
195	200	205	
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc			672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile			
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Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His			
225	230	235	240
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 65 70 75 80

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
 115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140

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Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
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Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
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Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp	
35 40 45	
atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa	192
Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln	
50 55 60	
aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat	240
Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His	
65 70 75 80	
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Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr	
85 90 95	
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Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys	
100 105 110	
aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat	384
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp	
115 120 125	
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Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile	
145 150 155 160	
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Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr	
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195 200 205	

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 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
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Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
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Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
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Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
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Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
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Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
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Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile						
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35 40 45	
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Tyr Ala Lys Ile His Lys Trp Leu Ile Pro Ile Ala Ile Val Trp Gln	
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Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys	
100 105 110	
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Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp	
115 120 125	
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Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile	
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Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His	
225 230 235 240	
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Tyr Ala Lys Ile His Lys Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
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Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
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Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110

Asn-His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
 115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140

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 145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
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Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
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Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
20 25 30

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Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
35 40 45

tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa 192
Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
50 55 60

atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat 240
Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
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85 90 95

cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag 336
Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
100 105 110

aat cat tgc tta cat cat cgt cat cct gct agc gat tta gac cca gat 384
Asn His Cys Leu His His Arg His Pro Ala Ser Asp Leu Asp Pro Asp
115 120 125

ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc	432
Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe	
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atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta	480
Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu	
145 150 155 160	
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc	528
Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile	
165 170 175	
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Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr	
180 185 190	
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ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc	672
Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile	
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Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His	
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gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac	768
Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn	
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aat tca gta acc aat tcg taa	789
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35 40 45

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
50 55 60

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
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Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Asp Leu Asp Pro Asp
115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
130 135 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
245 250 255

Asn Ser Val Thr Asn Ser
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<210> 11

<211> 762

<212> DNA

<213> Unknown

<220>

<221> CDS

<223> Artificial sequence

<400> 11

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gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96
Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
20 25 30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144
Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp
35 40 45

atc tca aag att cat aag tgg atg tta ttg cct gtt ata cta tgg caa 192
Ile Ser Lys Ile His Lys Trp Met Leu Leu Pro Val Ile Leu Trp Gln
50 55 60

aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240
Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
65 70 75 80

ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288
Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
85 90 95

ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa 336
Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
100 105 110

aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat 384
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
115 120 125

ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt 432
Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
130 135 140

atg	aaa	ggt	tac	tgg	agt	tgg	ggg	caa	ata	att	gcg	ttg	act	att	att	480
Met	Lys	Gly	Tyr	Trp	Ser	Trp	Gly	Gln	Ile	Ile	Ala	Leu	Thr	Ile	Ile	
145					150					155					160	

tat	aac	ttt	gct	aaa	tac	ata	ctc	cat	atc	cca	agt	gat	aat	cta	act	528
Tyr	Asn	Phe	Ala	Lys	Tyr	Ile	Leu	His	Ile	Pro	Ser	Asp	Asn	Leu	Thr	
				165					170					175		

tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat 576

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
 180 185 190

ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag 624
 Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205

cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc 672
 Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
 210 215 220

acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat 720
 Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag 762
 Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
 245 250

<210> 12
 <211> 253
 <212> PRT
 <213> Unknown
 <220>
 <223> Artificial sequence

<400> 12

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 1 5 10 15

Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
 35 40 45

Ile Ser Lys Ile His Lys Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys

100	105	110
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp		
115	120	125
Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe		
130	135	140
Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile		
145	150	155
Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr		
165	170	175
Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr		
180	185	190
Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln		
195	200	205
Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile		
210	215	220
Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His		
225	230	235
Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys		
245	250	

<210> 13

<211> 762

<212> DNA

<213> Unknown

<220>

<221> CDS

<223> Artificial sequence

<400> 13

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1 5 10 15	
gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc	96

Val	Leu	Arg	Ser	Lys	Ser	Gln	Phe	Lys	Gly	Leu	Phe	Ile	Ala	Ile	Val	
			20					25					30			
att	gtt	agc	gca	tgg	gtc	att	agc	ctg	agt	tta	tta	ctt	tcc	ctt	gac	144
Ile	Val	Ser	Ala	Trp	Val	Ile	Ser	Leu	Ser	Leu	Leu	Leu	Ser	Leu	Asp	
		35					40					45				
atc	tca	aag	cta	aaa	ttt	tgg	atg	tta	ttg	cct	gtt	ata	cta	tgg	caa	192
Ile	Ser	Lys	Leu	Lys	Phe	Trp	Met	Leu	Leu	Pro	Val	Ile	Leu	Trp	Gln	
		50				55				60						
aca	ttt	tta	tat	acg	gga	tta	ttt	att	aca	tct	cat	gat	gcc	atg	cat	240
Thr	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Ser	His	Asp	Ala	Met	His	
65					70					75					80	
ggc	gta	gta	ttt	ccc	caa	aac	acc	aag	att	aat	cat	ttg	att	gga	aca	288
Gly	Val	Val	Phe	Pro	Gln	Asn	Thr	Lys	Ile	Asn	His	Leu	Ile	Gly	Thr	
				85					90				95			
ttg	acc	cta	tcc	ctt	tat	ggg	ctt	tta	cca	tat	caa	aaa	cta	ttg	aaa	336
Leu	Thr	Leu	Ser	Leu	Tyr	Gly	Leu	Leu	Pro	Tyr	Gln	Lys	Leu	Leu	Lys	
			100					105					110			
aaa	cat	tgg	tta	cac	cac	cac	aat	cca	gca	agc	gat	tta	gac	ccg	gat	384
Lys	His	Trp	Leu	His	His	His	Asn	Pro	Ala	Ser	Asp	Leu	Asp	Pro	Asp	
		115					120					125				
ttt	cac	aat	ggg	aaa	cac	caa	agt	ttc	ttt	gct	tgg	tat	ttt	cat	ttt	432
Phe	His	Asn	Gly	Lys	His	Gln	Ser	Phe	Phe	Ala	Trp	Tyr	Phe	His	Phe	
	130					135					140					
atg	aaa	ggg	tac	tgg	agt	tgg	ggg	caa	ata	att	gcg	ttg	act	att	att	480
Met	Lys	Gly	Tyr	Trp	Ser	Trp	Gly	Gln	Ile	Ile	Ala	Leu	Thr	Ile	Ile	
145					150					155					160	
tat	aac	ttt	gct	aaa	tac	ata	ctc	cat	atc	cca	agt	gat	aat	cta	act	528
Tyr	Asn	Phe	Ala	Lys	Tyr	Ile	Leu	His	Ile	Pro	Ser	Asp	Asn	Leu	Thr	
				165					170					175		
tac	ttt	tgg	gtg	cta	ccc	tcg	ctt	tta	agt	tca	tta	caa	tta	ttc	tat	576
Tyr	Phe	Trp	Val	Leu	Pro	Ser	Leu	Leu	Ser	Ser	Leu	Gln	Leu	Phe	Tyr	
			180					185					190			
ttt	ggg	act	ttt	tta	ccc	cat	agt	gaa	cca	ata	ggg	ggg	tat	gtt	cag	624
Phe	Gly	Thr	Phe	Leu	Pro	His	Ser	Glu	Pro	Ile	Gly	Gly	Tyr	Val	Gln	
		195					200					205				
cct	cat	tgt	gcc	caa	aca	att	agc	cgt	cct	att	tgg	tgg	tca	ttt	atc	672
Pro	His	Cys	Ala	Gln	Thr	Ile	Ser	Arg	Pro	Ile	Trp	Trp	Ser	Phe	Ile	
		210				215					220					
acg	tgc	tat	cat	ttt	ggc	tac	cac	gag	gaa	cat	cac	gaa	tat	cct	cat	720
Thr	Cys	Tyr	His	Phe	Gly	Tyr	His	Glu	Glu	His	His	Glu	Tyr	Pro	His	
225					230					235				240		
att	tct	tgg	tgg	cag	tta	cca	gaa	att	tac	aaa	gca	aaa	tag			762
Ile	Ser	Trp	Trp	Gln	Leu	Pro	Glu	Ile	Tyr	Lys	Ala	Lys				
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<210> 14

<211> 253

<212> PRT

<213> Unknown

<220>

<223> Artificial sequence

<400> 14

Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
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Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
 35 40 45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
 100 105 110

Lys His Trp Leu His His His Asn Pro Ala Ser Asp Leu Asp Pro Asp
 115 120 125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
 130 135 140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
 145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
 165 170 175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr

180

185

190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
 210 215 220

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
 245 250

<210> 15

<211> 1608

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (3)..(971)

<400> 15

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 Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
 1 5 10 15

ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
 20 25 30

tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc 143
 Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala
 35 40 45

cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg 191
 Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser
 50 55 60

tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga 239
 Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly
 65 70 75

acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca 287
 Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala
 80 85 90 95

ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa 335

Leu	Gln	Gln	Leu	Asp	Arg	Ala	Ile	Ala	Glu	Arg	Arg	Ala	Arg	Lys	
				100					105					110	
cgg	gag	cag	ctg	tca	tac	cag	gct	gcc	gcc	att	gca	gca	tca	att	ggc
Arg	Glu	Gln	Leu	Ser	Tyr	Gln	Ala	Ala	Ala	Ile	Ala	Ala	Ser	Ile	Gly
			115					120					125		
gtg	tca	ggc	att	gcc	atc	ttc	gcc	acc	tac	ctg	aga	ttt	gcc	atg	cac
Val	Ser	Gly	Ile	Ala	Ile	Phe	Ala	Thr	Tyr	Leu	Arg	Phe	Ala	Met	His
		130					135					140			
atg	acc	gtg	ggc	ggc	gca	gtg	cca	tgg	ggt	gaa	gtg	gct	ggc	act	ctc
Met	Thr	Val	Gly	Gly	Ala	Val	Pro	Trp	Gly	Glu	Val	Ala	Gly	Thr	Leu
	145					150					155				
ctc	ttg	gtg	gtt	ggt	ggc	gcg	ctc	ggc	atg	gag	atg	tat	gcc	cgc	tat
Leu	Leu	Val	Val	Gly	Gly	Ala	Leu	Gly	Met	Glu	Met	Tyr	Ala	Arg	Tyr
160					165					170					175
gca	cac	aaa	gcc	atc	tgg	cat	gag	tcg	cct	ctg	ggc	tgg	ctg	ctg	cac
Ala	His	Lys	Ala	Ile	Trp	His	Glu	Ser	Pro	Leu	Gly	Trp	Leu	Leu	His
			180						185					190	
aag	agc	cac	cac	aca	cct	cgc	act	gga	ccc	ttt	gaa	gcc	aac	gac	ttg
Lys	Ser	His	His	Thr	Pro	Arg	Thr	Gly	Pro	Phe	Glu	Ala	Asn	Asp	Leu
			195					200					205		
ttt	gca	atc	atc	aat	gga	ctg	ccc	gcc	atg	ctc	ctg	tgt	acc	ttt	ggc
Phe	Ala	Ile	Ile	Asn	Gly	Leu	Pro	Ala	Met	Leu	Leu	Cys	Thr	Phe	Gly
		210					215					220			
ttc	tgg	ctg	ccc	aac	gtc	ctg	ggg	gcg	gcc	tgc	ttt	gga	gcg	ggg	ctg
Phe	Trp	Leu	Pro	Asn	Val	Leu	Gly	Ala	Ala	Cys	Phe	Gly	Ala	Gly	Leu
	225					230					235				
ggc	atc	acg	cta	tac	ggc	atg	gca	tat	atg	ttt	gta	cac	gat	ggc	ctg
Gly	Ile	Thr	Leu	Tyr	Gly	Met	Ala	Tyr	Met	Phe	Val	His	Asp	Gly	Leu
240					245					250				255	
gtg	cac	agg	cgc	ttt	ccc	acc	ggg	ccc	atc	gct	ggc	ctg	ccc	tac	atg
Val	His	Arg	Arg	Phe	Pro	Thr	Gly	Pro	Ile	Ala	Gly	Leu	Pro	Tyr	Met
				260					265					270	
aag	cgc	ctg	aca	gtg	gcc	cac	cag	cta	cac	cac	agc	ggc	aag	tac	ggt
Lys	Arg	Leu	Thr	Val	Ala	His	Gln	Leu	His	His	Ser	Gly	Lys	Tyr	Gly
			275					280					285		
ggc	gcg	ccc	tgg	ggt	atg	ttc	ttg	ggt	cca	cag	gag	ctg	cag	cac	att
Gly	Ala	Pro	Trp	Gly	Met	Phe	Leu	Gly	Pro	Gln	Glu	Leu	Gln	His	Ile
		290					295					300			
cca	ggt	gcg	gcg	gag	gag	gtg	gag	cga	ctg	gtc	ctg	gaa	ctg	gac	tgg
Pro	Gly	Ala	Ala	Glu	Glu	Val	Glu	Arg	Leu	Val	Leu	Glu	Leu	Asp	Trp
	305					310					315				
tcc	aag	cgg	tag	ggtgcggaac	caggcagcgt	ggttttcacac	ctcatgcctg								

tggccaatgg catcggccat gtctgggtcat cacgggctgg ttgcctgggt gaaggtgatg 1131
 cacatcatca tgtgcgggtg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc 1191
 caggctggcg ttgaatcagt gagggtttgt gattggcggt tgtgaagcaa tgactccgcc 1251
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 catgatgtac tcgtcatggt gtgttgggtga gaggatggat gtggatggat gtgtattctc 1431
 agacgtagac cttgactgga ggcttgatcg agagagtggg ccgtattctt tgagagggga 1491
 ggctcgtgcc agaaatggtg agtggatgac tgtgacgctg tacattgcag gcaggtgaga 1551
 tgcactgtct cgattgtaaa atacattcag atgcaaaaaa aaaaaaaaaa aaaaaaa 1608

<210> 16

<211> 322

<212> PRT

<213> Haematococcus pluvialis

<400> 16

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Pro	Pro	Pro	His	Leu	His	Arg	Ser	Phe	Ala	Ala	Thr	Thr	Met	Leu	Ser
			20					25					30		
Lys	Leu	Gln	Ser	Ile	Ser	Val	Lys	Ala	Arg	Arg	Val	Glu	Leu	Ala	Arg
		35					40					45			
Asp	Ile	Thr	Arg	Pro	Lys	Val	Cys	Leu	His	Ala	Gln	Arg	Cys	Ser	Leu
	50					55					60				
Val	Arg	Leu	Arg	Val	Ala	Ala	Pro	Gln	Thr	Glu	Glu	Ala	Leu	Gly	Thr
65				70						75				80	
Val	Gln	Ala	Ala	Gly	Ala	Gly	Asp	Glu	His	Ser	Ala	Asp	Val	Ala	Leu
			85						90					95	
Gln	Gln	Leu	Asp	Arg	Ala	Ile	Ala	Glu	Arg	Arg	Ala	Arg	Arg	Lys	Arg
		100						105					110		
Glu	Gln	Leu	Ser	Tyr	Gln	Ala	Ala	Ala	Ile	Ala	Ala	Ser	Ile	Gly	Val
		115						120					125		

Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met
 130 135 140

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu
 145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala
 165 170 175

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys
 180 185 190

Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe
 195 200 205

Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe
 210 215 220

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly
 225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val
 245 250 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys
 260 265 270

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
 275 280 285

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
 290 295 300

Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
 305 310 315 320

Lys Arg

<210> 17

<211> 1650

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (112) .. (1614)

<400> 17

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aggaccccat ttgaagtttt cttgaaacaa atattaccct gttggaaaaa g atg gat      117
                                   Met Asp
                                   1

act ttg ttg aaa acc cca aat aac ctt gaa ttt ctg aac cca cat cat      165
Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro His His
      5                               10                               15

ggg ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat cat aat      213
Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His His Asn
      20                               25                               30

ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt tgt gtt      261
Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val Cys Val
      35                               40                               45                               50

aag ggt agt agt agt gct ctt tta gag ctt gta cct gag acc aaa aag      309
Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr Lys Lys
      55                               60                               65

gag aat ctt gat ttt gag ctt cct atg tat gac cct tca aaa ggg gtt      357
Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys Gly Val
      70                               75                               80

gtt gtg gat ctt gct gtg gtt ggt ggt ggc cct gca gga ctt gct gtt      405
Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu Ala Val
      85                               90                               95

gca cag caa gtt tct gaa gca gga ctc tct gtt tgt tca att gat cgg      453
Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile Asp Pro
      100                               105                               110

aat cct aaa ttg ata tgg cct aat aac tat ggt gtt tgg gtg gat gaa      501
Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
      115                               120                               125                               130

ttt gag gct atg gac ttg tta gat tgt cta gat gct acc tgg tct ggt      549
Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp Ser Gly
      135                               140                               145

gca gca gtg tac att gat gat aat acg gct aaa gat ctt cat aga cct      597
Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His Arg Pro
      150                               155                               160

tat gga agg gtt aac cgg aaa cag ctg aaa tcg aaa atg atg cag aaa      645
Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met Gln Lys
      165                               170                               175

tgt ata atg aat ggt gtt aaa ttc cac caa gcc aaa gtt ata aag gtg      693

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Cys	Ile	Met	Asn	Gly	Val	Lys	Phe	His	Gln	Ala	Lys	Val	Ile	Lys	Val	
180						185					190					
att	cat	gag	gaa	tcg	aaa	tcc	atg	ttg	ata	tgc	aat	gat	ggg	att	act	741
Ile	His	Glu	Glu	Ser	Lys	Ser	Met	Leu	Ile	Cys	Asn	Asp	Gly	Ile	Thr	
195					200					205					210	
att	cag	gca	acg	gtg	gtg	ctc	gat	gca	act	ggc	ttc	tct	aga	tct	ctt	789
Ile	Gln	Ala	Thr	Val	Val	Leu	Asp	Ala	Thr	Gly	Phe	Ser	Arg	Ser	Leu	
				215					220					225		
gtt	cag	tat	gat	aag	cct	tat	aac	ccc	ggg	tat	caa	gtt	gct	tat	ggc	837
Val	Gln	Tyr	Asp	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Gln	Val	Ala	Tyr	Gly	
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Ile	Leu	Ala	Glu	Val	Glu	Glu	His	Pro	Phe	Asp	Val	Asn	Lys	Met	Val	
		245					250					255				
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Phe	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Lys	Asn	Asn	Thr	Asp	Leu	Lys	
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Glu	Arg	Asn	Ser	Arg	Ile	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Ser	
275					280					285					290	
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Ser	Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	Pro	Gly	
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Leu	Arg	Ile	Asp	Asp	Ile	Gln	Glu	Arg	Met	Val	Ala	Arg	Leu	Asn	His	
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		325					330					335				
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Pro	Met	Gly	Gly	Pro	Leu	Pro	Val	Leu	Pro	Gln	Arg	Val	Val	Gly	Ile	
	340					345					350					
ggg	ggg	aca	gct	ggc	atg	gtt	cat	cca	tcc	acc	ggg	tat	atg	gtg	gca	1221
Gly	Gly	Thr	Ala	Gly	Met	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val	Ala	
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agg	aca	cta	gct	gcg	gct	cct	gtt	gtt	gcc	aat	gcc	ata	att	caa	tac	1269
Arg	Thr	Leu	Ala	Ala	Ala	Pro	Val	Val	Ala	Asn	Ala	Ile	Ile	Gln	Tyr	
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Leu	Gly	Ser	Glu	Arg	Ser	His	Ser	Gly	Asn	Glu	Leu	Ser	Thr	Ala	Val	
			390					395					400			
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Trp	Lys	Asp	Leu	Trp	Pro	Ile	Glu	Arg	Arg	Arg	Gln	Arg	Glu	Phe	Phe	
		405					410					415				
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Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala Thr Arg
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 Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp His Gly
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 Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe Gly Leu
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 Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile Met Thr
 470 475 480
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 Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu Gln Asp
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 Lys Glu
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<212> PRT

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His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val
 35 40 45

Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
 50 55 60

Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
 65 70 75 80

Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
 85 90 95

Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile
 100 105 110

Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val
 115 120 125

Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp
 130 135 140

Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His
 145 150 155 160

Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met
 165 170 175

Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile
 180 185 190

Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly
 195 200 205

Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg
 210 215 220

Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala
 225 230 235 240

Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys
 245 250 255

Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp
 260 265 270

Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro
 275 280 285

Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg
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Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu
 305 310 315 320

Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys
 325 330 335

Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val
 340 345 350

Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met
 355 360 365

Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile
 370 375 380

Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr
 385 390 395 400

Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
 405 410 415

Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
 420 425 430

Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
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His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe
 450 455 460

Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
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Gln Asp Lys Glu
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<212> DNA

<213> Unknown

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<223> Artificial sequence

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<213> Nostoc sp. Strain PCC7120

<220>

<221> variation

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ttatcttatt tttatgggca attagtttaa tcttattact ctcaatagat acatccataa 180

ttcataagag cttattaggt atagccatgc tttggcagac cttcttatat acaggtttat 240

ttattactgc tcatgatgcc atgcacggcg tagtttatcc caaaaatccc agaataaata 300

attttatagg taagctcact ctaatcttgt atggactact cccttataaa gatttattga 360

aaaaacattg gttacaccac ggacatcctg gtactgattt agaccctgat tattacaatg 420

gtcatcccca aaacttcttt ctttgggtatc tacattttat gaagtcttat tggcgatgga 480

cgcaaatttt cggattagtg atgatttttc atggacttaa aaatctgggtg catataccag 540

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attttggtac atttttgcct cataaaaagc tagaaggtgg ttataactaac cccattgtg 660

cgcgcagtat cccattacct cttttttggt cttttgttac ttgttatcac ttcggctacc 720

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tatctttata aggtctagag catgc 805

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<211> 24

<212> DNA

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24

<210> 23

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<213> Unknown

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<223> Artificial sequence

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26

<210> 24

<211> 4624

<212> DNA

<213> Erwinia uredovora

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<220>

<221> CDS

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<222> (2802) .. (3689)

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agcggct atg caa ccg cat tat gat ctg att ctc gtg ggg gct gga ctc      169
    Met Gln Pro His Tyr Asp Leu Ile Leu Val Gly Ala Gly Leu
        1             5             10

gcg aat ggc ctt atc gcc ctg cgt ctt cag cag cag caa cct gat atg      217
Ala Asn Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln Gln Pro Asp Met
15             20             25             30

cgt att ttg ctt atc gac gcc gca ccc cag gcg ggc ggg aat cat acg      265
Arg Ile Leu Leu Ile Asp Ala Ala Pro Gln Ala Gly Gly Asn His Thr
        35             40             45

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Trp Ser Phe His His Asp Asp Leu Thr Glu Ser Gln His Arg Trp Ile
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gct ccg ctg gtg gtt cat cac tgg ccc gac tat cag gta cgc ttt ccc      361
Ala Pro Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro
        65             70             75

aca cgc cgt cgt aag ctg aac agc ggc tac ttt tgt att aat tct cag      409
Thr Arg Arg Arg Lys Leu Asn Ser Gly Tyr Phe Cys Ile Thr Ser Gln
        80             85             90

cgt ttc gct gag gtt tta cag cga cag ttt ggc ccg cac ttg tgg atg      457
Arg Phe Ala Glu Val Leu Gln Arg Gln Phe Gly Pro His Leu Trp Met
        95             100            105            110

gat acc gcg gtc gca gag gtt aat gcg gaa tct gtt cgg ttg aaa aag      505
Asp Thr Ala Val Ala Glu Val Asn Ala Glu Ser Val Arg Leu Lys Lys
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ggg cag gtt atc ggt gcc cgc gcg gtg att gac ggg cgg ggt tat gcg      553
Gly Gln Val Ile Gly Ala Arg Ala Val Ile Asp Gly Arg Gly Tyr Ala
        130            135            140

gca aat tca gca ctg agc gtg ggc ttc cag gcg ttt att ggc cag gaa      601
Ala Asn Ser Ala Leu Ser Val Gly Phe Gln Ala Phe Ile Gly Gln Glu
        145            150            155

tgg cga ttg agc cac ccg cat ggt tta tcg tct ccc att atc atg gat      649
Trp Arg Leu Ser His Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp
        160            165            170

gcc acg gtc gat cag caa aat ggt tat cgc ttc gtg tac agc ctg ccg      697
Ala Thr Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Ser Leu Pro

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Leu Ser Pro Thr Arg Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Asn				
	195	200	205	
gcg aca tta gat cct gaa tgc gcg cgg caa aat att tgc gac tat gcc				793
Ala Thr Leu Asp Pro Glu Cys Ala Arg Gln Asn Ile Cys Asp Tyr Ala				
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Ala Gln Gln Gly Trp Gln Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly				
	225	230	235	
gcc tta ccc att act ctg tgc ggc aat gcc gac gca ttc tgg cag cag				889
Ala Leu Pro Ile Thr Leu Ser Gly Asn Ala Asp Ala Phe Trp Gln Gln				
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cgc ccc ctg gcc tgt agt gga tta cgt gcc ggt ctg ttc cat cct acc				937
Arg Pro Leu Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr				
	255	260	265	270
acc ggc tat tca ctg ccg ctg gcg gtt gcc gtg gcc gac cgc ctg agt				985
Thr Gly Tyr Ser Leu Pro Leu Ala Val Ala Val Ala Asp Arg Leu Ser				
	275	280	285	
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Ala Leu Asp Val Phe Thr Ser Ala Ser Ile His His Ala Ile Thr His				
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Phe Ala Arg Glu Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn				
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cgc atg ctg ttt tta gcc gga ccc gcc gat tca cgc tgg cgg gtt atg				1129
Arg Met Leu Phe Leu Ala Gly Pro Ala Asp Ser Arg Trp Arg Val Met				
	320	325	330	
cag cgt ttt tat ggt tta cct gaa gat tta att gcc cgt ttt tat gcg				1177
Gln Arg Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala				
	335	340	345	350
gga aaa ctc acg ctg acc gat cgg cta cgt att ctg agc ggc aag ccg				1225
Gly Lys Leu Thr Leu Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro				
	355	360	365	
cct gtt ccg gta tta gca gca ttg caa gcc att atg acg act				1267
Pro Val Pro Val Leu Ala Ala Leu Gln Ala Ile Met Thr Thr				
	370	375	380	
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Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe				
	385	390		
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Gly Gly Leu Ala Leu Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val				
	395	400	405	
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Leu Leu Leu Glu Gln Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr				

410	415	420	
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caa ctg gcg aaa ctg cag gca tgg aga agc gtt tac agt aag gtt gcc Gln Leu Ala Lys Leu Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala 540 545 550			1800
agt tac atc gaa gat gaa cat ctg cgc cag gcg ttt tct ttc cac tcg Ser Tyr Ile Glu Asp Glu His Leu Arg Gln Ala Phe Ser Phe His Ser 555 560 565			1848
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650	655	660	
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Leu Ser Gln His Pro Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr			
665	670	675	
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Lys Arg Met Ser Asn Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His			
680	685	690	695
cat cat gat cag ctc gcg cat cac acg gtt tgt ttc ggc ccg cgt tac			2280
His His Asp Gln Leu Ala His His Thr Val Cys Phe Gly Pro Arg Tyr			
700	705	710	
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Arg Glu Leu Ile Asp Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp			
715	720	725	
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Phe Ser Leu Tyr Leu His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala			
730	735	740	
cct gaa ggt tgc ggc agt tac tat gtg ttg gcg ccg gtg ccg cat tta			2424
Pro Glu Gly Cys Gly Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu			
745	750	755	
ggc acc gcg aac ctc gac tgg acg gtt gag ggg cca aaa cta cgc gac			2472
Gly Thr Ala Asn Leu Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp			
760	765	770	775
cgt att ttt gcg tac ctt gag cag cat tac atg cct ggc tta cgg agt			2520
Arg Ile Phe Ala Tyr Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser			
780	785	790	
cag ctg gtc acg cac cgg atg ttt acg ccg ttt gat ttt cgc gac cag			2568
Gln Leu Val Thr His Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln			
795	800	805	
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Leu Asn Ala Tyr His Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr			
810	815	820	
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Gln Ser Ala Trp Phe Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn			
825	830	835	
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Leu Tyr Leu Val Gly Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly			
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Val Ile Gly Ser Ala Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu			
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Ile		Met Ala Val Gly	
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Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr Arg			

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Ala Trp Asp Gln Arg Gln	Ser Thr Thr Thr Pro	Glu Lys Leu Thr	
1125	1130	1135	
ctg ctg ctg gcc gcc tct	ggt cag gcc ctt act	tcc cgg atg cgg	3647
Leu Leu Leu Ala Ala Ser	Gly Gln Ala Leu Thr	Ser Arg Met Arg	
1140	1145	1150	
gct cat cct ccc cgc cct	gcg cat ctc tgg cag	cgc ccg ctc	3689
Ala His Pro Pro Arg Pro	Ala His Leu Trp Gln	Arg Pro Leu	
1155	1160	1165	
tagcgccatg tctttcccg agcgtcgct gaagttttga caggggcggc gcatagagga			3749
agccaaaaga aacacaacct tctttgcccc tgacggcgtg atgcatacgg tgcgccatat			3809
acaaccgttt gaggtagccc ttgctggaa tatagcggaa tggccaacgt tgatgcacca			3869
gcccgtcgtg caccataaaa tagagtaatc catacgccgt catacctgcg ccaatccact			3929
ggagcggcca cattcctgta ctgccagat aaatcagcag gatcgataat gcagcaaaaa			3989
ccacggcata aagatcgta acttcaaacy cacctttacg cggttcatga tgtgaaagat			4049
gccatcccca accccagccg tgcgatgatgt atttgtgtgc cagtgcagca atcacttcca			4109
tgccaatcac ggtaacgaaa acgatcaggg cattccaaat ccacaacata atttctccgg			4169
tagagacgtc tggcagcagg ctttaaggatt caattttaac agagattagc cgatctggcg			4229
gcgggaaggg aaaaaggcgc gccagaaagg cgcgccaggg atcagaagtc ggctttcaga			4289
aecacacggt agttggcttt acctgcacga acatgggtcca gtgcatcggt gattttcgac			4349
atcgggaagt actccactgt cggcgcaata tctgtacggc cagccagctt cagcagtga			4409
cgcagctgcg caggtgaacc ggttgaagaa cccgtcacgg cgcggtcgcc taaaatcagg			4469
ctgaaagccg ggcacgtcaa acggcttcag tacggcacc acggtatgga acttaccgcg			4529
aggcgccagg gccgcaaagt agggttgcc gtcgagatcg acggcgaccg tgctgataat			4589
caggtcaaac tggcccgcca ggctttttta agctt			4624

<210> 25

<211> 380

<212> PRT

<213> Erwinia uredovora

<400> 25

Met	Gln	Pro	His	Tyr	Asp	Leu	Ile	Leu	Val	Gly	Ala	Gly	Leu	Ala	Asn
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Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln Gln Pro Asp Met Arg Ile
20 25 30

Leu Leu Ile Asp Ala Ala Pro Gln Ala Gly Gly Asn His Thr Trp Ser
35 40 45

Phe His His Asp Asp Leu Thr Glu Ser Gln His Arg Trp Ile Ala Pro
50 55 60

Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Thr Arg
65 70 75 80

Arg Arg Lys Leu Asn Ser Gly Tyr Phe Cys Ile Thr Ser Gln Arg Phe
85 90 95

Ala Glu Val Leu Gln Arg Gln Phe Gly Pro His Leu Trp Met Asp Thr
100 105 110

Ala Val Ala Glu Val Asn Ala Glu Ser Val Arg Leu Lys Lys Gly Gln
115 120 125

Val Ile Gly Ala Arg Ala Val Ile Asp Gly Arg Gly Tyr Ala Ala Asn
130 135 140

Ser Ala Leu Ser Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Arg
145 150 155 160

Leu Ser His Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
165 170 175

Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Ser Leu Pro Leu Ser
180 185 190

Pro Thr Arg Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Asn Ala Thr
195 200 205

Leu Asp Pro Glu Cys Ala Arg Gln Asn Ile Cys Asp Tyr Ala Ala Gln
210 215 220

Gln Gly Trp Gln Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
225 230 235 240

Pro Ile Thr Leu Ser Gly Asn Ala Asp Ala Phe Trp Gln Gln Arg Pro
245 250 255

Leu Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
 260 265 270

Tyr Ser Leu Pro Leu Ala Val Ala Val Ala Asp Arg Leu Ser Ala Leu
 275 280 285

Asp Val Phe Thr Ser Ala Ser Ile His His Ala Ile Thr His Phe Ala
 290 295 300

Arg Glu Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
 305 310 315 320

Leu Phe Leu Ala Gly Pro Ala Asp Ser Arg Trp Arg Val Met Gln Arg
 325 330 335

Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
 340 345 350

Leu Thr Leu Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
 355 360 365

Pro Val Leu Ala Ala Leu Gln Ala Ile Met Thr Thr
 370 375 380

<210> 26

<211> 492

<212> PRT

<213> Erwinia uredovora

<400> 26

Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
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Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30

Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe
 35 40 45

Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60

Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu

65		70		75		80
Leu Pro Val Thr	Pro Phe Tyr Arg	Leu Cys Trp Glu Ser Gly Lys Val				
	85	90			95	
Phe Asn Tyr Asp	Asn Asp Gln Thr Arg	Leu Glu Ala Gln Ile Gln Gln				
	100	105			110	
Phe Asn Pro Arg	Asp Val Glu Gly Tyr Arg	Gln Phe Leu Asp Tyr Ser				
	115	120			125	
Arg Ala Val Phe	Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe					
	130	135			140	
Leu Ser Phe Arg	Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu					
	145	150			155	160
Gln Ala Trp Arg	Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp					
	165	170			175	
Glu His Leu Arg	Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly					
	180	185			190	
Asn Pro Phe Ala	Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu					
	195	200			205	
Arg Glu Trp Gly	Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val					
	210	215			220	
Gln Gly Met Ile	Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu					
	225	230			235	240
Asn Ala Arg Val	Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala					
	245	250			255	
Val His Leu Glu	Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser					
	260	265			270	
Asn Ala Asp Val	Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro					
	275	280			285	
Ala Ala Val Lys	Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn					
	290	295			300	
Ser Leu Phe Val	Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu					

305 310 315 320
 Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp
 325 330 335
 Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
 340 345 350
 His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly
 355 360 365
 Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
 370 375 380
 Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr
 385 390 395 400
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
 420 425 430
 Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
 435 440 445
 Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
 450 455 460
 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
 485 490

 <210> 27
 <211> 296
 <212> PRT
 <213> Erwinia uredovora
 <400> 27
 Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp
 1 5 10 15

Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
20 25 30

Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln
35 40 45

Pro Ala Leu Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys
50 55 60

Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
65 70 75 80

Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
85 90 95

Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr
100 105 110

Ser Gln Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
115 120 125

Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
130 135 140

Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
145 150 155 160

Ala Arg Asp Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro
165 170 175

Ala Ser Trp Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala
180 185 190

Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln
195 200 205

Glu Ala Glu Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu
210 215 220

Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
225 230 235 240

Lys Ile Gly Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln
245 250 255

Arg Gln Ser Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala
 260 265 270

Ser Gly Gln Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro
 275 280 285

Ala His Leu Trp Gln Arg Pro Leu
 290 295

<210> 28

<211> 32

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Artificial sequence

<400> 28

tttttctcga gcgataaacg ctcaattggt ta

32

<210> 29

<211> 32

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Artificial sequence

<400> 29

tttttgtcga cacgttatgc tcacaacccc gg

32

<210> 30

<211> 679

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (87)..(635)

<400> 30

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ctcgagcgcgat aaacgctcac ttgggttaatc atttcactct tcaattatct ataatgatga      60
gtgatcagaa ttacatgtga gaaatt atg caa acg gaa cac gtc att tta ttg      113
      Met Gln Thr Glu His Val Ile Leu Leu
      1                      5

aat gca cag gga gtt ccc acg ggt acg ctg gaa aag tat gcc gca cac      161
Asn Ala Gln Gly Val Pro Thr Gly Thr Leu Glu Lys Tyr Ala Ala His
10                      15                      20                      25

acg gca gac acc cgc tta cat ctc gcg ttc tcc agt tgg ctg ttt aat      209
Thr Ala Asp Thr Arg Leu His Leu Ala Phe Ser Ser Trp Leu Phe Asn
      30                      35                      40

gcc aaa gga caa tta tta gtt acc cgc cgc gca ctg agc aaa aaa gca      257
Ala Lys Gly Gln Leu Leu Val Thr Arg Arg Ala Leu Ser Lys Lys Ala
      45                      50                      55

tgg cct ggc gtg tgg act aac tcg gtt tgt ggg cac cca caa ctg gga      305
Trp Pro Gly Val Trp Thr Asn Ser Val Cys Gly His Pro Gln Leu Gly
      60                      65                      70

gaa agc aac gaa gac gca gtg atc cgc cgt tgc cgt tat gag ctt ggc      353
Glu Ser Asn Glu Asp Ala Val Ile Arg Arg Cys Arg Tyr Glu Leu Gly
      75                      80                      85

gtg gaa att acg cct cct gaa tct atc tat cct gac ttt cgc tac cgc      401
Val Glu Ile Thr Pro Pro Glu Ser Ile Tyr Pro Asp Phe Arg Tyr Arg
      90                      95                      100                      105

gcc acc gat ccg agt ggc att gtg gaa aat gaa gtg tgt ccg gta ttt      449
Ala Thr Asp Pro Ser Gly Ile Val Glu Asn Glu Val Cys Pro Val Phe
      110                      115                      120

gcc gca cgc acc act agt gcg tta cag atc aat gat gat gaa gtg atg      497
Ala Ala Arg Thr Thr Ser Ala Leu Gln Ile Asn Asp Asp Glu Val Met
      125                      130                      135

gat tat caa tgg tgt gat tta gca gat gta tta cac ggt att gat gcc      545
Asp Tyr Gln Trp Cys Asp Leu Ala Asp Val Leu His Gly Ile Asp Ala
      140                      145                      150

acg ccg tgg gcg ttc agt ccg tgg atg gtg atg cag gcg aca aat cgc      593
Thr Pro Trp Ala Phe Ser Pro Trp Met Val Met Gln Ala Thr Asn Arg
      155                      160                      165

gaa gcc aga aaa cga tta tct gca ttt acc cag ctt aaa taa      635
Glu Ala Arg Lys Arg Leu Ser Ala Phe Thr Gln Leu Lys
      170                      175                      180

aaaaaccccg acatttgccg gggttgtgag cataacgtgt cgac      679

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<210> 31

<211> 182

<212> PRT

<213> Escherichia coli

<400> 31

Met Gln Thr Glu His Val Ile Leu Leu Asn Ala Gln Gly Val Pro Thr
1 5 10 15

Gly Thr Leu Glu Lys Tyr Ala Ala His Thr Ala Asp Thr Arg Leu His
20 25 30

Leu Ala Phe Ser Ser Trp Leu Phe Asn Ala Lys Gly Gln Leu Leu Val
35 40 45

Thr Arg Arg Ala Leu Ser Lys Lys Ala Trp Pro Gly Val Trp Thr Asn
50 55 60

Ser Val Cys Gly His Pro Gln Leu Gly Glu Ser Asn Glu Asp Ala Val
65 70 75 80

Ile Arg Arg Cys Arg Tyr Glu Leu Gly Val Glu Ile Thr Pro Pro Glu
85 90 95

Ser Ile Tyr Pro Asp Phe Arg Tyr Arg Ala Thr Asp Pro Ser Gly Ile
100 105 110

Val Glu Asn Glu Val Cys Pro Val Phe Ala Ala Arg Thr Thr Ser Ala
115 120 125

Leu Gln Ile Asn Asp Asp Glu Val Met Asp Tyr Gln Trp Cys Asp Leu
130 135 140

Ala Asp Val Leu His Gly Ile Asp Ala Thr Pro Trp Ala Phe Ser Pro
145 150 155 160

Trp Met Val Met Gln Ala Thr Asn Arg Glu Ala Arg Lys Arg Leu Ser
165 170 175

Ala Phe Thr Gln Leu Lys
180

<210> 32

<211> 31

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Artificial sequence

<400> 32

tttttccatg gtgaaggagg aaatagcgaa a

31

<210> 33

<211> 32

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Artificial sequence

<400> 33

tttttaagct ttcacttttt tcttgtaacc aa

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<210> 34

<211> 962

<212> DNA

<213> Archaeoglobus fulgidus

<220>

<221> CDS

<222> (3)..(956)

<400> 34

cc atg gtg aag gag gaa ata gcg aaa agg gcc gaa ata atc aac aaa
Met Val Lys Glu Glu Ile Ala Lys Arg Ala Glu Ile Ile Asn Lys
1 5 10 15

47

gcc att gaa gag ctt ctg ccc gaa agg gag ccg att gga ctc tac aaa
Ala Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys
20 25 30

95

gcc gca agg cat ctg atc aaa gca ggt ggc aag agg cta agg cct gta
Ala Ala Arg His Leu Ile Lys Ala Gly Lys Arg Leu Arg Pro Val
35 40 45

143

ata agc ctc tta gca gtc gaa gcc ctt ggg aaa gac tac aga aag att
Ile Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile

191

50	55	60	
atc ccg gct gct gtc agc att gaa aca atc cac aac ttc acc ctc gtg Ile Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val 65 70 75			239
cat gac gac ata atg gac agg gac gag atg agg agg gga gtt ccg acg His Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr 80 85 90 95			287
gta cac agg gtt tat ggg gaa gcg acg gcc att tta gca ggc gac aca Val His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr 100 105 110			335
ctc ttt gct gaa gcc ttc aag ctg ctg aca aag tgc gat gtt gag agc Leu Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser 115 120 125			383
gag gga atc aga aaa gct aca gaa atg ctt tcg gac gtt tgc ata aaa Glu Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys 130 135 140			431
ata tgc gag ggg cag tac tac gac atg agc ttt gag aaa aag gag agc Ile Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser 145 150 155			479
gtt tcc gag gag gag tat ctc agg atg gtc gag ctg aag acc gga gtg Val Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val 160 165 170 175			527
ctg att gca gct tct gca gca tta cct gcg gtg ctt ttt ggg gag agc Leu Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser 180 185 190			575
gag gaa att gta aag gcg ctg tgg gac tac gga gtt ctt agc ggt att Glu Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile 195 200 205			623
ggc ttc cag atc cag gac gac ctg ctt gac ctg act gag gag acc gga Gly Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly 210 215 220			671
aag gac tgg gga agc gac ctg ctt aaa ggg aag aaa acc ctg att gtc Lys Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val 225 230 235			719
ata aag gcg ttc gaa aag gga gtg aag cta aag acg ttt gga aag gaa Ile Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu 240 245 250 255			767
aag gcg gac gtc tct gag att aga gat gat atc gaa aag tta aga gag Lys Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu 260 265 270			815
tgt ggt gcg att gat tac gct gcc agc atg gca aga aag atg gct gaa Cys Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu 275 280 285			863
gag gcg aaa aga aag ctc gaa gtt ctg cct gaa agc aaa gcc aag gaa Glu Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu			911

290	295	300	
aca ctg ctg gaa ctt acc gac ttc ttg gtt aca aga aaa aag tga			956
Thr Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys			
305	310	315	
aagctt			962
<210>	35		
<211>	317		
<212>	PRT		
<213>	Archaeoglobus fulgidus		
<400>	35		
Met Val Lys Glu Glu Ile Ala Lys Arg Ala Glu Ile Ile Asn Lys Ala			
1	5	10	15
Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys Ala			
	20	25	30
Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val Ile			
	35	40	45
Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile Ile			
	50	55	60
Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val His			
65	70	75	80
Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr Val			
	85	90	95
His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr Leu			
	100	105	110
Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser Glu			
	115	120	125
Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys Ile			
	130	135	140
Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser Val			
145	150	155	160
Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val Leu			

	165		170		175										
Ile	Ala	Ala	Ser	Ala	Ala	Leu	Pro	Ala	Val	Leu	Phe	Gly	Glu	Ser	Glu
			180					185					190		
Glu	Ile	Val	Lys	Ala	Leu	Trp	Asp	Tyr	Gly	Val	Leu	Ser	Gly	Ile	Gly
		195					200					205			
Phe	Gln	Ile	Gln	Asp	Asp	Leu	Leu	Asp	Leu	Thr	Glu	Glu	Thr	Gly	Lys
	210					215					220				
Asp	Trp	Gly	Ser	Asp	Leu	Leu	Lys	Gly	Lys	Lys	Thr	Leu	Ile	Val	Ile
225					230					235					240
Lys	Ala	Phe	Glu	Lys	Gly	Val	Lys	Leu	Lys	Thr	Phe	Gly	Lys	Glu	Lys
			245					250						255	
Ala	Asp	Val	Ser	Glu	Ile	Arg	Asp	Asp	Ile	Glu	Lys	Leu	Arg	Glu	Cys
		260					265						270		
Gly	Ala	Ile	Asp	Tyr	Ala	Ala	Ser	Met	Ala	Arg	Lys	Met	Ala	Glu	Glu
	275						280					285			
Ala	Lys	Arg	Lys	Leu	Glu	Val	Leu	Pro	Glu	Ser	Lys	Ala	Lys	Glu	Thr
	290					295					300				
Leu	Leu	Glu	Leu	Thr	Asp	Phe	Leu	Val	Thr	Arg	Lys	Lys			
305					310					315					

<210> 36

<211> 1293

<212> DNA

<213> Archaeoglobus fulgidus

<220>

<221> CDS

<222> (206)..(1159)

<400> 36

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gccccccctc gacgccgtcg ttcaatgaga atggataaga ggctcgtggg attgacgtga 120

gggggcaggg atggctatat ttctgggagc gaactccggg cgaggatcta gttgtaggga 180

gggattcatg acaccacaaa cagcc	atg gtg aag gag gaa ata gcg aaa agg	232
	Met Val Lys Glu Glu Ile Ala Lys Arg	
	1 5	
gcc gaa ata atc aac aaa gcc att gaa gag ctt ctg ccc gaa agg gag	280	
Ala Glu Ile Ile Asn Lys Ala Ile Glu Glu Leu Leu Pro Glu Arg Glu		
10 15 20 25		
ccg att gga ctc tac aaa gcc gca agg cat ctg atc aaa gca ggt ggc	328	
Pro Ile Gly Leu Tyr Lys Ala Ala Arg His Leu Ile Lys Ala Gly Gly		
	30 35 40	
aag agg cta agg cct gta ata agc ctc tta gca gtc gaa gcc ctt ggg	376	
Lys Arg Leu Arg Pro Val Ile Ser Leu Leu Ala Val Glu Ala Leu Gly		
	45 50 55	
aaa gac tac aga aag att atc ccg gct gct gtc agc att gaa aca atc	424	
Lys Asp Tyr Arg Lys Ile Ile Pro Ala Ala Val Ser Ile Glu Thr Ile		
	60 65 70	
cac aac ttc acc ctc gtg cat gac gac ata atg gac agg gac gag atg	472	
His Asn Phe Thr Leu Val His Asp Asp Ile Met Asp Arg Asp Glu Met		
	75 80 85	
agg agg gga gtt ccg acg gta cac agg gtt tat ggg gaa gcg acg gcc	520	
Arg Arg Gly Val Pro Thr Val His Arg Val Tyr Gly Glu Ala Thr Ala		
90 95 100 105		
att tta gca ggc gac aca ctc ttt gct gaa gcc ttc aag ctg ctg aca	568	
Ile Leu Ala Gly Asp Thr Leu Phe Ala Glu Ala Phe Lys Leu Leu Thr		
	110 115 120	
aag tgc gat gtt gag agc gag gga atc aga aaa gct aca gaa atg ctt	616	
Lys Cys Asp Val Glu Ser Glu Gly Ile Arg Lys Ala Thr Glu Met Leu		
	125 130 135	
tcg gac gtt tgc ata aaa ata tgc gag ggg cag tac tac gac atg agc	664	
Ser Asp Val Cys Ile Lys Ile Cys Glu Gly Gln Tyr Tyr Asp Met Ser		
	140 145 150	
ttt gag aaa aag gag agc gtt tcc gag gag gag tat ctc agg atg gtc	712	
Phe Glu Lys Lys Glu Ser Val Ser Glu Glu Glu Tyr Leu Arg Met Val		
	155 160 165	
gag ctg aag acc gga gtg ctg att gca gct tct gca gca tta cct gcg	760	
Glu Leu Lys Thr Gly Val Leu Ile Ala Ala Ser Ala Ala Leu Pro Ala		
170 175 180 185		
gtg ctt ttt ggg gag agc gag gaa att gta aag gcg ctg tgg gac tac	808	
Val Leu Phe Gly Glu Ser Glu Glu Ile Val Lys Ala Leu Trp Asp Tyr		
	190 195 200	
gga gtt ctt agc ggt att ggc ttc cag atc cag gac gac ctg ctt gac	856	
Gly Val Leu Ser Gly Ile Gly Phe Gln Ile Gln Asp Asp Leu Leu Asp		
	205 210 215	
ctg act gag gag acc gga aag gac tgg gga agc gac ctg ctt aaa ggg	904	
Leu Thr Glu Glu Thr Gly Lys Asp Trp Gly Ser Asp Leu Leu Lys Gly		
	220 225 230	

aag aaa acc ctg att gtc ata aag gcg ttc gaa aag gga gtg aag cta 952
 Lys Lys Thr Leu Ile Val Ile Lys Ala Phe Glu Lys Gly Val Lys Leu
 235 240 245

aag acg ttt gga aag gaa aag gcg gac gtc tct gag att aga gat gat 1000
 Lys Thr Phe Gly Lys Glu Lys Ala Asp Val Ser Glu Ile Arg Asp Asp
 250 255 260 265

atc gaa aag tta aga gag tgt ggt gcg att gat tac gct gcc agc atg 1048
 Ile Glu Lys Leu Arg Glu Cys Gly Ala Ile Asp Tyr Ala Ala Ser Met
 270 275 280

gca aga aag atg gct gaa gag gcg aaa aga aag ctc gaa gtt ctg cct 1096
 Ala Arg Lys Met Ala Glu Glu Ala Lys Arg Lys Leu Glu Val Leu Pro
 285 290 295

gaa agc aaa gcc aag gaa aca ctg ctg gaa ctt acc gac ttc ttg gtt 1144
 Glu Ser Lys Ala Lys Glu Thr Leu Leu Glu Leu Thr Asp Phe Leu Val
 300 305 310

aca aga aaa aag tga aagcttcaat tgcattgctct agatgatcaa agaattcctg 1199
 Thr Arg Lys Lys
 315

gcctagtcta taggagggttt tgaaaagaaa ggagcaataa tcattttctt gttctatcaa 1259

gagggtgcta ttgctccttt ctttttttct cgag 1293

<210> 37

<211> 317

<212> PRT

<213> Archaeoglobus fulgidus

<400> 37

Met Val Lys Glu Glu Ile Ala Lys Arg Ala Glu Ile Ile Asn Lys Ala
 1 5 10 15

Ile Glu Glu Leu Leu Pro Glu Arg Glu Pro Ile Gly Leu Tyr Lys Ala
 20 25 30

Ala Arg His Leu Ile Lys Ala Gly Gly Lys Arg Leu Arg Pro Val Ile
 35 40 45

Ser Leu Leu Ala Val Glu Ala Leu Gly Lys Asp Tyr Arg Lys Ile Ile
 50 55 60

Pro Ala Ala Val Ser Ile Glu Thr Ile His Asn Phe Thr Leu Val His
 65 70 75 80

Asp Asp Ile Met Asp Arg Asp Glu Met Arg Arg Gly Val Pro Thr Val

85

90

95

His Arg Val Tyr Gly Glu Ala Thr Ala Ile Leu Ala Gly Asp Thr Leu
 100 105 110

Phe Ala Glu Ala Phe Lys Leu Leu Thr Lys Cys Asp Val Glu Ser Glu
 115 120 125

Gly Ile Arg Lys Ala Thr Glu Met Leu Ser Asp Val Cys Ile Lys Ile.
 130 135 140

Cys Glu Gly Gln Tyr Tyr Asp Met Ser Phe Glu Lys Lys Glu Ser Val
 145 150 155 160

Ser Glu Glu Glu Tyr Leu Arg Met Val Glu Leu Lys Thr Gly Val Leu
 165 170 175

Ile Ala Ala Ser Ala Ala Leu Pro Ala Val Leu Phe Gly Glu Ser Glu
 180 185 190

Glu Ile Val Lys Ala Leu Trp Asp Tyr Gly Val Leu Ser Gly Ile Gly
 195 200 205

Phe Gln Ile Gln Asp Asp Leu Leu Asp Leu Thr Glu Glu Thr Gly Lys
 210 215 220

Asp Trp Gly Ser Asp Leu Leu Lys Gly Lys Lys Thr Leu Ile Val Ile
 225 230 235 240

Lys Ala Phe Glu Lys Gly Val Lys Leu Lys Thr Phe Gly Lys Glu Lys
 245 250 255

Ala Asp Val Ser Glu Ile Arg Asp Asp Ile Glu Lys Leu Arg Glu Cys
 260 265 270

Gly Ala Ile Asp Tyr Ala Ala Ser Met Ala Arg Lys Met Ala Glu Glu
 275 280 285

Ala Lys Arg Lys Leu Glu Val Leu Pro Glu Ser Lys Ala Lys Glu Thr
 290 295 300

Leu Leu Glu Leu Thr Asp Phe Leu Val Thr Arg Lys Lys
 305 310 315

<211> 35
 <212> DNA
 <213> Unknown
 <220>
 <221> primer_bind
 <223> Artificial sequence
 <400> 38
 gagctcttca ttatttcgat ttgatttcg tgacc 35

<210> 39
 <211> 38
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Primer
 <400> 39
 aagcttggtt gatcagaaga agaagaagaa gatgaact 38

<210> 40
 <211> 647
 <212> DNA
 <213> Arabidopsis thaliana
 <220>
 <221> Promoter
 <400> 40
 gagctcttca ttatttcgat ttgatttcg tgaccagcga acgcagaata ccttggttg 60
 taatacttta cccgtgtaaa tcaaaaacaa aaaggctttt gagctttttg tagttgaatt 120
 tctctggctg atcttttctg tacagattca tatatctgca gagacgatat cattgattat 180
 ttgagcttct tttgaactat ttcgtgtaat ttgggatgag agctctatgt atgtgtgtaa 240
 actttgaaga caacaagaaa ggtaacaagt gagggaggga tgactccatg tcaaataga 300
 tgtcataaga ggcccatcaa taagtgcttg agccattag ctagccagat aactaccaga 360
 ttgtgagatg gatgtgtgaa cagttttttt ttgatgtag gactgaaatg tgaacaacag 420

gcgcatgaaa ggctaaatta ggacaatgat aagcagaaat aacttatacct ctctaact 480
 tggcctcaca ttgcccttca cacaatccac acacatccaa tcacaacctc atcatatatc 540
 tcccgcataat ctttttttct ttgatctttt tttttttgct tattattttt ttgactttga 600
 tctcccatca gttcatcttc ttcttcttct tctgatcaac caagctt 647

<210> 41

<211> 28

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Artificial sequence

<400> 41

gagctcactc actgatttcc attgcttg 28

<210> 42

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 42

aagcttttgt tgaagagatt tgg 23

<210> 43

<211> 37

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Artificial sequence

<400> 43

cgccgttaag tcgatgtccg ttgatttaaa cagtgtc 37

<210> 44

<211> 34

<212> DNA

<213> Unknown

<220>

<221> primer_bind

<223> Artificial sequence

<400> 44

atcaacggac atcgacttaa cggcgtttgt aaac

34

<210> 45

<211> 777

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> Promoter

<400> 45

gagctcactc actgatttcc attgcttgaa aattgatgat gaactaagat caatccatgt	60
tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactgggtoga	120
agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagtttagga	180
ccaaacatta tctacaaaca aagacttttc tctaacttg tgattccttc ttaaacccta	240
ggggtaatat tctattttcc aaggatcttt agttaaggc aaatccggga aattattgta	300
atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca	360
tatatatctc tttctttctta tttcccaaata taacagacaa aagtagaata ttggctttta	420
acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca	480
aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccggt aagtcgatgt	540
ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta	600
tcacttagtt ttcatcaact tctgaactta cttttcatgg attaggcaat actttccatt	660
tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact	720
tctttcttct cattatatct cttgtcctct ccaccaaata tcttcaacaa aaagctt	777

<210> 46

<211> 804

<212> DNA

<213> Synechococcus WH8102

<220>

<221> CDS

<400> 46

atg aaa acg aca aga tct att tcg tgg cca tcg act tgc tgg cat cac	48
Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His	
1 5 10 15	
cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc	96
Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala	
20 25 30	
ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc	144
Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu	
35 40 45	
tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg	192
Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu	
50 55 60	
ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg	240
Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu	
65 70 75 80	
ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat	288
Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His	
85 90 95	
ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca	336
Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala	
100 105 110	
ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac ctg	384
Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu	
115 120 125	
gca ccg gag acg ttc cag gat cct gac tac caa cgt tgc acc aat aac	432
Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn	
130 135 140	
aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg	480
Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met	
145 150 155 160	
cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc	528
Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu	
165 170 175	

aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc 576
Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
180 185 190

gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc 624
Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
195 200 205

tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg 672
Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
210 215 220

cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac 720
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
 225 230 235 240

ttt	ggc	tat	cat	cgt	gaa	cat	cat	gaa	tgc	cct	tcc	aca	ccc	tgg	ttt	768
Phe	Gly	Tyr	His	Arg	Glu	His	His	Glu	Ser	Pro	Ser	Thr	Pro	Trp	Phe	.
				245				250						255		

cag ctg cca caa ctt cga aat gaa tca ttc act tga 804
Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
260 265

<210> 47

<211> 267

<212> PRT

<213> Synechococcus WH8102

<400> • 47

Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
1 5 10 15

Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
20 25 30

Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
35 40 45

Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
50 55 60

Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu
65 70 75 80

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
85 90 95

Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
 100 105 110

Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu
 115 120 125

Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
 130 135 140

Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
 145 150 155 160

Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
 165 170 175

Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
 180 185 190

Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
 195 200 205

Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
 210 215 220

Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
 225 230 235 240

Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
 245 250 255

Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
 260 265

<210> 48

<211> 804

<212> DNA

<213> Unknown

<220>

<221> CDS

<223> Artificial variant

<400> 48

atg aaa acg aca aga tct att tcg tgg cca tcg act tgc tgg cat cac

Met	Lys	Thr	Thr	Arg	Ser	Ile	Ser	Trp	Pro	Ser	Thr	Cys	Trp	His	His	
1				5					10					15		
cag	ccg	agt	tgc	tca	agc	tgg	gtg	gca	aat	gag	ttc	agc	cct	cag	gcc	96
Gln	Pro	Ser	Cys	Ser	Ser	Trp	Val	Ala	Asn	Glu	Phe	Ser	Pro	Gln	Ala	
			20					25					30			
ctc	aaa	ggg	ttg	gct	ctg	gct	ggc	ctg	att	gga	tca	gcc	tgg	ctg	ctc	144
Leu	Lys	Gly	Leu	Ala	Leu	Ala	Gly	Leu	Ile	Gly	Ser	Ala	Trp	Leu	Leu	
		35					40					45				
tcc	ctg	ggc	ctg	agc	tac	acc	ctg	cca	ctt	gat	cag	acg	cct	ggg	ctg	192
Ser	Leu	Gly	Leu	Ser	Tyr	Thr	Leu	Pro	Leu	Asp	Gln	Thr	Pro	Gly	Leu	
		50				55					60					
ttg	att	ggc	agc	ttg	att	ctg	tgg	cag	acc	ttt	ctg	cac	acc	ggg	ctg	240
Leu	Ile	Gly	Ser	Leu	Ile	Leu	Trp	Gln	Thr	Phe	Leu	His	Thr	Gly	Leu	
65					70					75					80	
ttc	atc	gtt	gcc	cac	gat	tcc	atg	cac	gcc	agt	ctg	gtt	ccg	ggc	cat	288
Phe	Ile	Val	Ala	His	Asp	Ser	Met	His	Ala	Ser	Leu	Val	Pro	Gly	His	
				85					90						95	
ccc	gga	ttg	aac	cgc	tgg	atc	ggc	aaa	gtg	tat	ttg	ttg	gtg	tat	gca	336
Pro	Gly	Leu	Asn	Arg	Trp	Ile	Gly	Lys	Val	Tyr	Leu	Leu	Val	Tyr	Ala	
			100					105					110			
ggc	ttg	tct	tat	gag	cgt	tgt	tcc	cgc	aac	cac	aga	cgt	cat	cac	ctg	384
Gly	Leu	Ser	Tyr	Glu	Arg	Cys	Ser	Arg	Asn	His	Arg	Arg	His	His	Leu	
		115					120					125				
gca	ccg	gag	acg	ttc	cag	gat	cct	gac	tac	caa	cgt	tgc	acc	aat	aac	432
Ala	Pro	Glu	Thr	Phe	Gln	Asp	Pro	Asp	Tyr	Gln	Arg	Cys	Thr	Asn	Asn	
			130				135				140					
aac	atc	cta	gat	tgg	tat	gtt	cac	ttc	atg	ggc	aac	tat	ctg	ggc	atg	480
Asn	Ile	Leu	Asp	Trp	Tyr	Val	His	Phe	Met	Gly	Asn	Tyr	Leu	Gly	Met	
145					150					155					160	
cgg	caa	ctg	tta	aat	cta	agc	tgt	ctt	tgg	ctg	gcg	cta	atc	att	ctc	528
Arg	Gln	Leu	Leu	Asn	Leu	Ser	Cys	Leu	Trp	Leu	Ala	Leu	Ile	Ile	Leu	
				165					170					175		
aac	ggc	tct	gat	ctc	cct	gct	cag	atc	atg	cat	ctg	ctg	ttg	ttc	agc	576
Asn	Gly	Ser	Asp	Leu	Pro	Ala	Gln	Ile	Met	His	Leu	Leu	Leu	Phe	Ser	
			180					185					190			
gtt	ctg	ccg	ttg	atc	atc	agt	tcc	tgt	caa	ttg	ttt	cta	gtg	gga	acc	624
Val	Leu	Pro	Leu	Ile	Ile	Ser	Ser	Cys	Gln	Leu	Phe	Leu	Val	Gly	Thr	
		195					200					205				
tgg	tta	ccc	cac	cga	cgt	ggg	gcc	acg	aca	cga	ccg	ggc	gtg	aca	acg	672
Trp	Leu	Pro	His	Arg	Arg	Gly	Ala	Thr	Thr	Arg	Pro	Gly	Val	Thr	Thr	
		210				215					220					
cgc	agc	ctg	gct	ttg	cat	cca	gcc	ctc	tct	ttc	gca	gct	tgt	tac	aac	720
Arg	Ser	Leu	Ala	Leu	His	Pro	Ala	Leu	Ser	Phe	Ala	Ala	Cys	Tyr	Asn	
225					230					235					240	
ttt	ggc	tat	cat	cgt	gaa	cat	cat	gaa	tcg	cct	tcc	aca	ccc	tgg	ttt	768

Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
245 250 255

cag ctg cca caa ctt cga aat gaa tca ttc act tga
Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
260 265

804

<210> 49

<211> 267

<212> PRT

<213> Unknown

<220>

<223> Artificial variant

<400> 49

Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
1 5 10 15

Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
 20 25 30

Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
35 40 45

Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
50 55 60

Leu Ile Gly Ser Leu Ile Leu Trp Gln Thr Phe Leu His Thr Gly Leu
65 70 75 80

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
85 90 95

Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
100 105 110

Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu
115 120 125

Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
130 135 140

Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
145 150 155 160

Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
165 170 175

Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
180 185 190

Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
195 200 205

Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
210 215 220

Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
225 230 235 240

Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
245 250 255

Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
260 265

<210> 50

<211> 804

<212> DNA

<213> Unknown

<220>

<221> CDS

<223> Artificial variant

<400> 50

atg aaa acg aca aga tct att tcg tgg cca tcg act tgc tgg cat cac 48
Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
1 5 10 15

cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96
Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
20 25 30

ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc 144
Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
35 40 45

tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg 192
Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
50 55 60

ttg	att	ggc	agc	ttg	att	ctg	ctc	aga	gca	ttt	ctg	cac	acc	ggg	ctg		240
Leu	Ile	Gly	Ser	Leu	Ile	Leu	Leu	Arg	Ala	Phe	Leu	His	Thr	Gly	Leu		
65					70					75					80		
ttc	atc	gtt	gcc	cac	gat	tcc	atg	cac	gcc	agt	ctg	gtt	ccg	ggc	cat		288
Phe	Ile	Val	Ala	His	Asp	Ser	Met	His	Ala	Ser	Leu	Val	Pro	Gly	His		
				85					90					95			
ccc	gga	ttg	aac	cgc	tgg	atc	ggc	aaa	gtg	tat	ttg	ttg	gtg	tat	gca		336
Pro	Gly	Leu	Asn	Arg	Trp	Ile	Gly	Lys	Val	Tyr	Leu	Leu	Val	Tyr	Ala		
			100					105					110				
ggc	ttg	tct	tat	gag	cgt	tgt	tcc	cgc	aac	cac	aga	cgt	cat	cac	gga		384
Gly	Leu	Ser	Tyr	Glu	Arg	Cys	Ser	Arg	Asn	His	Arg	Arg	His	His	Gly		
		115					120					125					
cat	cct	ggc	act	gat	tta	gat	cct	gac	tac	caa	cgt	tgc	acc	aat	aac		432
His	Pro	Gly	Thr	Asp	Leu	Asp	Pro	Asp	Tyr	Gln	Arg	Cys	Thr	Asn	Asn		
	130					135					140						
aac	atc	cta	gat	tgg	tat	gtt	cac	ttc	atg	ggc	aac	tat	ctg	ggc	atg		480
Asn	Ile	Leu	Asp	Trp	Tyr	Val	His	Phe	Met	Gly	Asn	Tyr	Leu	Gly	Met		
145					150					155					160		
cgg	caa	ctg	tta	aat	cta	agc	tgt	ctt	tgg	ctg	gcg	cta	atc	att	ctc		528
Arg	Gln	Leu	Leu	Asn	Leu	Ser	Cys	Leu	Trp	Leu	Ala	Leu	Ile	Ile	Leu		
				165					170					175			
aac	ggc	tct	gat	ctc	cct	gct	cag	atc	atg	cat	ctg	ctg	ttg	ttc	agc		576
Asn	Gly	Ser	Asp	Leu	Pro	Ala	Gln	Ile	Met	His	Leu	Leu	Leu	Phe	Ser		
			180					185					190				
gtt	ctg	ccg	ttg	atc	atc	agt	tcc	tgt	caa	ttg	ttt	cta	gtg	gga	acc		624
Val	Leu	Pro	Leu	Ile	Ile	Ser	Ser	Cys	Gln	Leu	Phe	Leu	Val	Gly	Thr		
		195					200					205					
tgg	tta	ccc	cac	cga	cgt	ggg	gcc	acg	aca	cga	ccg	ggc	gtg	aca	acg		672
Trp	Leu	Pro	His	Arg	Arg	Gly	Ala	Thr	Thr	Arg	Pro	Gly	Val	Thr	Thr		
	210					215					220						
cgc	agc	ctg	gct	ttg	cat	cca	gcc	ctc	tct	ttc	gca	gct	tgt	tac	aac		720
Arg	Ser	Leu	Ala	Leu	His	Pro	Ala	Leu	Ser	Phe	Ala	Ala	Cys	Tyr	Asn		
225					230					235					240		
ttt	ggc	tat	cat	cgt	gaa	cat	cat	gaa	tcg	cct	tcc	aca	ccc	tgg	ttt		768
Phe	Gly	Tyr	His	Arg	Glu	His	His	Glu	Ser	Pro	Ser	Thr	Pro	Trp	Phe		
				245				250						255			
cag	ctg	cca	caa	ctt	cga	aat	gaa	tca	ttc	act	tga						804
Gln	Leu	Pro	Gln	Leu	Arg	Asn	Glu	Ser	Phe	Thr							
			260			</											

<210> 51

<211> 267

<212> PRT

<213> Unknown

<220>

<223> Artificial variant

<400> 51

Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
1 5 10 15

Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
20 25 30

Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
35 40 45

Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
50 55 60

Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu
65 70 75 80

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
85 90 95

Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
100 105 110

Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Gly
115 120 125

His Pro Gly Thr Asp Leu Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
130 135 140

Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
145 150 155 160

Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
165 170 175

Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
180 185 190

Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
195 200 205

Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
210 215 220

Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
225 230 235 240

Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
245 250 255

Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
260 265

<210> 52

<211> 690

<212> DNA

<213> Nodularia spumigena NSOR10

<220>

<221> CDS

<400> 52

atg gcg atc gcc att att agt ata tgg gct atc agc cta ggt ttg tta	48
Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu	
1 5 10 15	
ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc	96
Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu	
20 25 30	
ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat	144
Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His	
35 40 45	
gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat	192
Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His	
50 55 60	
ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa	240
Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln	
65 70 75 80	
aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa	288
Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu	
85 90 95	
aca gat cca gat ttt cac aac ggg aag cag aaa aac ttt ttt gct tgg	336
Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp	
100 105 110	
tat tta tat ttt atg aag cgt tac tgg agt tgg tta caa att atc aca	384
Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr	
115 120 125	

tta atg att att tat aac tta cta aaa tat ata tgg cat ttt cca gag 432
 Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu
 130 135 140

gat aat atg act tat ttt tgg gta gtt ccc tca att tta agt tct tta 480
 Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu
 145 150 155 160

caa tta ttt tat ttt gga act ttt cta ccc cac agt gag cct gta gaa 528
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu
 165 170 175

ggt tat aaa gag cct cat cgt tcc caa act att agc cgt ccc att tgg 576
 Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp
 180 185 190

tgg tca ttt ata act tgt tac cat ttt ggt tat cat tac gaa cat cat 624
 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His
 195 200 205

gaa tac ccc cat gtt cct tgg tgg caa tta cca gaa att tat aaa atg 672
 Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met
 210 215 220

tct aaa tca aat ttg tga 690
 Ser Lys Ser Asn Leu
 225

<210> 53

<211> 229

<212> • PRT

<213> Nodularia spumigena NSOR10

<400> 53

Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu
 1 5 10 15

Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
 20 25 30

Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 35 40 45

Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His
 50 55 60

Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln
 65 70 75 80

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu
 85 90 95

Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp
 100 105 110

Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr
 115 120 125

Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu
 130 135 140

Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu
 145 150 155 160

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu
 165 170 175

Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp
 180 185 190

Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His
 195 200 205

Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met
 210 215 220

Ser Lys Ser Asn Leu
 225

<210> 54

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 54

gcgcatgcat ctagaaatga tccagttaga acaacca

37

<210> 55

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 55

gcgc atgctc tagactat ttt tgctttgtaa atttctg

37

<210> 56

<211> 792

<212> DNA

<213> Nostoc punctiforme ATCC 29133

<220>

<221> CDS

<222> (5)..(775)

<400> 56

gcgc atg cat cta gaa atg atc cag tta gaa caa cca ctc agt cat caa
Met His Leu Glu Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln
1 5 10 15

49

gca aaa ctg act cca gta ctg aga agt aaa tct cag ttt aag ggg ctt
Ala Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu
20 25 30

97

ttc att gct att gtc att gtt agc gca tgg gtc att agc ctg agt tta
Phe Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu
35 40 45

145

tta ctt tcc ctt gac atc tca aag cta aaa ttt tgg atg tta ttg cct
Leu Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro
50 55 60

193

gtt ata cta tgg caa aca ttt tta tat acg gga tta ttt att aca tct
Val Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser
65 70 75

241

cat gat gcc atg cat ggc gta gta ttt ccc caa aac acc aag att aat
His Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn
80 85 90 95

289

cat ttg att gga aca ttg acc cta tcc ctt tat ggt ctt tta cca tat
His Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr
100 105 110

337

caa aaa cta ttg aaa aaa cat tgg tta cac cac cac aat cca gca agc
Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser
115 120 125

385

tca ata gac ccg gat ttt cac aat ggt aaa cac caa agt ttc ttt gct 433
 Ser Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala
 130 135 140

tgg tat ttt cat ttt atg aaa ggt tac tgg agt tgg ggg caa ata att 481
 Trp Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile
 145 150 155

gcg ttg act att att tat aac ttt gct aaa tac ata ctc cat atc cca 529
 Ala Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro
 160 165 170 175

agt gat aat cta act tac ttt tgg gtg cta ccc tcg ctt tta agt tca 577
 Ser Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser
 180 185 190

tta caa tta ttc tat ttt ggt act ttt tta ccc cat agt gaa cca ata 625
 Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile
 195 200 205

ggg ggt tat gtt cag cct cat tgt gcc caa aca att agc cgt cct att 673
 Gly Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile
 210 215 220

tgg tgg tca ttt atc acg tgc tat cat ttt ggc tac cac gag gaa cat 721
 Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His
 225 230 235

cac gaa tat cct cat att tct tgg tgg cag tta cca gaa att tac aaa 769
 His Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys
 240 245 250 255

gca aaa tagtctagag catgcgc 792
 Ala Lys

<210> 57

<211> 257

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 57

Met His Leu Glu Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala
 1 5 10 15

Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe
 20 25 30

Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu
 35 40 45

Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val

50

55

60

Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His
65 70 75 80

Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His
85 90 95

Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln
100 105 110

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Ser
115 120 125

Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp
130 135 140

Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala
145 150 155 160

Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser
165 170 175

Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu
180 185 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly
195 200 205

Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp
210 215 220

Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His
225 230 235 240

Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala
245 250 255

Lys

<210> 58

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 58

gtcgaccctg ctttaatgag atatgc

26

<210> 59

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 59

ctcgagcttg gacaatcagt aaattga

27

<210> 60

<211> 210

<212> DNA

<213> Agrobacterium tumefaciens

<220>

<221> Terminator

<400> 60

gtcgaccctg ctttaatgag atatgagaga cgctatgat cgcattgatatt ttgctttcaa

60

ttctgttgtg caggttgtaa aaaacctgag catgtgtagc tcagatcctt accgccggtt

120

tcggttcatt ctaatgaata tatcaccctg tactatcgta tttttatgaa taatattctc

180

cgttcaattt actgattgtc caagctcgag

210

<210> 61

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 61

cccgggaatt cttcattatt tcgattttga tttcgtg

37

<210> 62

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 62

aagcttggtt gatcagaaga agaagaagaa gatgaact

38

<210> 63

<211> 652

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> Promoter

<400> 63

cccgggaatt cttcattatt tcgattttga tttcgtgacc agcgaacgca gaataccttg 60

ttgtgtaata ctttaccctt gtaaatacaa aacaaaaagg cttttgagct ttttgtagtt 120

gaatttctct ggctgatctt ttctgtacag attcatatat ctgcagagac gatatcattg 180

attatttgag cttcttttga actatttcgt gtaatttggg atgagagctc tatgtatgtg 240

tgtaaacttt gaagacaaca agaaaggtaa caagtgaggg agggatgact ccatgtcaaa 300

atagatgtca taagaggccc atcaataagt gcttgagccc attagctagc ccagtaacta 360

ccagattgtg agatggatgt gtgaacagtt ttttttttga tgtaggactg aaatgtgaac 420

aacaggcgca tgaaaggcta aattaggaca atgataagca gaaataactt atcctctcta 480

acacttggcc tcacattgcc cttcacacaa tccacacaca tccaatcaca acctcatcat 540

atatctcccg ctaatctttt tttctttgat cttttttttt ttgcttatta tttttttgac 600

tttgatctcc catcagttca tcttcttctt cttcttctga tcaaccaagc tt 652

<210> 64

<211> 29
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Primer
 <400> 64
 gagctctagc gcaatcttat gtggtacaa 29

<210> 65
 <211> 29
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Primer
 <400> 65
 aagcttttct tgaaagtaaa gattgagtc 29

<210> 66
 <211> 1773
 <212> DNA
 <213> Petunia hybrida
 <220>
 <221> Promoter
 <222> (1) .. (1773)
 <400> 66
 gagctctagc gcaatcttat gtggtacaaa tcttgattag tcgggaaaaa atgatgtggc 60
 cctacaaatg gttggaggat gggagatttg gctctatcta gagttatgtg gttggtgaag 120
 catttggtta ctctctgctg tggtagttgg catatocaca ttgtctcctt ccacttttat 180
 gacaattacg tgaaagttat gggttgtttt gtctattttt gtcgaggcct ttcttttctt 240
 tccaggttgt tgaagatggg ccaattcgat tagaataatg ttttgagctt tagcatattc 300
 tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat 360
 tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg 420
 tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct 480

actaacatat actagtaaag agaattattaa catggcacat ataatttgat gcaaaatgag 540
 tatgatgaaa tttaaaccaca aaatctcttg attttgacag tgtcaccttg acttggttaac 600
 taataagtca tgttttagtg gcagaaagac aaactcatcc accaactgta tagcaataaa 660
 aaatagaaga atcttcctga ggcaaagttt tggaaaaatt aagagtggct gagatttaac 720
 ttcaacagga attagttcca cttaactttt aggttacgat acagtgctaa ttaaataact 780
 taattgtatt agatatttct tgcacctaaa aaatttaaaa actgaaaaaa ggtagcaatc 840
 aaaataaaca aaaggacaaa ataagtgaag ggtacagcca ccaaccctgg cggctcactg 900
 tttgttggtt aaaacgtaga cttacaccta ccaaaatcta caactaaaat gaggcaataa 960
 tactttgccc aaaattacca agaaaagaaa aagaaaggaa tcccttaata ttactctcct 1020
 ccatttcaca ataaatatcc tagtttgact taaattagag tttaaaaaat gaaagacgac 1080
 ttttaaaact tgtaatctaa aataaatcat agttaaatgt gtggctataa atcattgtat 1140
 taacggtaaa gtggttaagt taaaagttaa ttgttttcaa atataaaaatt gtactatcat 1200
 tctttttgga atggactaat aagaaaacta tgacatccat tatggagcgg agggagtatc 1260
 tccttttaac aataaccttt gtcccttcaa ttcaattatc agtatgcaaa cattaaaaat 1320
 tattattgat gttaagtacc acatcatcct taatgataga atcatcgtag aacgcttttc 1380
 caggcacaca ttcaaactag ttagaccagt accacacatc gaatattcca gacttctttg 1440
 tttgaatagt cgactacatt ggataatgga acttctcgaa ttaacttcga attagtcgag 1500
 cccaaaataa tatatacgtc ggggtgaaaa ctataaaatg tttgacaaaa atgtcaaatt 1560
 aatatatcaa tctgcaacaa ccttttcacc ttgagaacac agctgaaatt ttttaciaag 1620
 gtagttggtg aagctagtca gcgaatccca ttaccttcca ctctacctaa ccccttcac 1680
 caacaacaaa tttctgtaat ttaaaaacta gccaaaaaag aactctcttt taciaagagc 1740
 caaagactca atctttactt tcaagaaaag ctt 1773

<210> 67

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 67

gcgcagcat ctagaatga atttttgtga taaaccagt

39

<210> 68

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 68

gcgc atgctc tagattacga attggttact gaattgt

37

<210> 69

<211> 819

<212> DNA

<213> Nostoc punctiforme ATCC 29133

<220>

<221> CDS

<222> (5)..(802)

<400> 69

gcgc atg cat cta gaa atg aat ttt tgt gat aaa cca gtt agc tat tat
 Met His Leu Glu Met Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr
 1 5 10 15

49

gtt gca ata gag caa tta agt gct aaa gaa gat act gtt tgg ggg ctg
 Val Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu
 20 25 30

97

gtg att gtc ata gta att att agt ctt tgg gta gct agt ttg gct ttt
 Val Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe
 35 40 45

145

tta cta gct att aat tat gcc aaa gtc cca att tgg ttg ata cct att
 Leu Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile
 50 55 60

193

gca ata gtt tgg caa atg ttc ctt tat aca ggg cta ttt att act gca
 Ala Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala
 65 70 75

241

cat gat gct atg cat ggg tca gtt tat cgt aaa aat ccc aaa att aat
 His Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn
 80 85 90 95

289

aat ttt atc ggt tca cta gct gta gcg ctt tac gct gtg ttt cca tat 337
 Asn Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr
 100 105 110

caa cag atg tta aag aat cat tgc tta cat cat cgt cat cct gct agc 385
 Gln Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser
 115 120 125

gaa gtt gac cca gat ttt cat gat ggt aag aga aca aac gct att ttc 433
 Glu Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe
 130 135 140

tgg tat ctc cat ttc atg ata gaa tac tcc agt tgg caa cag tta ata 481
 Trp Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile
 145 150 155

gta cta act atc cta ttt aat tta gct aaa tac gtt ttg cac atc cat 529
 Val Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His
 160 165 170 175

caa ata aat ctc atc tta ttt tgg agt att cct cca att tta agt tcc 577
 Gln Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser
 180 185 190

att caa ctg ttt tat ttc gga aca ttt ttg cct cat cga gaa ccc aag 625
 Ile Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys
 195 200 205

aaa gga tat gtt tat ccc cat tgc agc caa aca ata aaa ttg cca act 673
 Lys Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr
 210 215 220

ttt ttg tca ttt atc gct tgc tac cac ttt ggt tat cat gaa gaa cat 721
 Phe Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His
 225 230 235

cat gag tat ccc cat gta cct tgg tgg caa ctt cca tct gta tat aag 769
 His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys
 240 245 250 255

cag aga gta ttc aac aat tca gta acc aat tcg taatctagag catgcgc 819
 Gln Arg Val Phe Asn Asn Ser Val Thr Asn Ser
 260 265

<210> 70

<211> 266

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 70

Met His Leu Glu Met Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val
 1 5 10 15

Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val
20 25 30

Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu
35 40 45

Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala
50 55 60

Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
65 70 75 80

Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn
85 90 95

Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln
100 105 110

Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser Glu
115 120 125

Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp
130 135 140

Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val
145 150 155 160

Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln
165 170 175

Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile
180 185 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys
195 200 205

Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe
210 215 220

Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His
225 230 235 240

Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln
245 250 255

Arg Val Phe Asn Asn Ser Val Thr Asn Ser

260

265

<210> 71

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 71

gcgcatgcat ctagaaatgg cgatcgccat tat

33

<210> 72

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 72

gcgcatgcte tagatcacaa atttgattta ga

32

<210> 73

<211> 720

<212> DNA

<213> Nodularia spumigena NSOR10

<220>

<221> CDS

<222> (5)..(703)

<400> 73

gcgc atg cat cta gaa atg gcg atc gcc att att agt ata tgg gct atc

49

Met His Leu Glu Met Ala Ile Ala Ile Ser Ile Trp Ala Ile

1

5

10

15

agc cta ggt ttg tta ctt tat att gat ata tcc caa ttc aag ttt tgg

97

Ser Leu Gly Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp

20

25

30

atg ttg tta ccg ctc ata ttt tgg caa aca ttt tta tat acg gga tta Met Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu 35 40 45	145
ttt att aca gct cat gat gcc atg cat ggg gta gtt ttt ccc aaa aat Phe Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn 50 55 60	193
ccc aaa atc aac cat ttc att ggc tca ttg tgc ctg ttt ctt tat ggt Pro Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly 65 70 75	241
ctt tta cct tat caa aaa ctt tta aaa aag cat tgg cta cat cac cat Leu Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His 80 85 90 95	289
aat cca gcc agt gaa aca gat cca gat ttt cac aac ggg aag cag aaa Asn Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys 100 105 110	337
aac ttt ttt gct tgg tat tta tat ttt atg aag cgt tac tgg agt tgg Asn Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp 115 120 125	385
tta caa att atc aca tta atg att att tat aac tta cta aaa tat ata Leu Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile 130 135 140	433
tgg cat ttt cca gag gat aat atg act tat ttt tgg gta gtt ccc tca Trp His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser 145 150 155	481
att tta agt tct tta caa tta ttt tat ttt gga act ttt cta ccc cac Ile Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His 160 165 170 175	529
agt gag cct gta gaa ggt tat aaa gag cct cat cgt tcc caa act att Ser Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile 180 185 190	577
agc cgt ccc att tgg tgg tca ttt ata act tgt tac cat ttt ggt tat Ser Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr 195 200 205	625
cat tac gaa cat cat gaa tac ccc cat gtt cct tgg tgg caa tta cca His Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro 210 215 220	673
gaa att tat aaa atg tct aaa tca aat ttg tgatctagag catgcgc Glu Ile Tyr Lys Met Ser Lys Ser Asn Leu 225 230	720

<210> 74

<211> 233

<212> PRT

<213> Nodularia spumigena NSOR10

<400> 74

Met His Leu Glu Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser
 1 5 10 15

Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met
 20 25 30

Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe
 35 40 45

Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro
 50 55 60

Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu
 65 70 75 80

Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn
 85 90 95

Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn
 100 105 110

Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu
 115 120 125

Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp
 130 135 140

His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile
 145 150 155 160

Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser
 165 170 175

Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser
 180 185 190

Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His
 195 200 205

Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu
 210 215 220

Ile Tyr Lys Met Ser Lys Ser Asn Leu

225

230

79